SEQUENCE LISTING

<110> Abbott Laboratories
      Mukerji, Pradip
      Huang, Yung-Sheng
      Das, Tapas
      Thurmond, Jennifer M.
      Pereira, Suzette L.

<120> DESATURASE GENES AND USES THEREOF

<130> 6763.US.P1

<140> 10/054,534
<141> 2002-01-22

<150> US 09/769,863
<151> 2001-01-25

<160> 55

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO834

<221> misc_feature
<222> (3)...(3)
<223> b = g or c or t/u at position 3

<221> misc_feature
<222> (6)...(6)
<223> y = t/u or c at position 6

<221> misc_feature
<222> (9)...(9)
<223> y = t/u or c at position 9

<221> misc_feature
<222> (12)...(12)
<223> b = g or c or t/u at position 12

<221> misc_difference
<222> (18)...(18)
<223> r = g or a at position 18

<221> misc_feature
<222> (24)...(24)
<223> b = g or c or t/u at position 24

```
<221> misc_feature
<222> (30)...(30)
<223> y = t/u or c at position 30

<221> misc_feature
<222> (33)...(33)
<223> y = t/u or c at position 33

<221> misc_feature
<222> (36)...(36)
<223> b = g or c or t/u at position 36

<221> misc_feature
<222> (39)...(39)
<223> h = a or c or t/u at position 39

<221> misc_feature
<222> (42)...(42)
<223> h = a or c or t/u at position 42

<400> 1
gtbtaygayg tbaccgartg ggtbaagcgy cayccbgghg gh                    42

<210> 2
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer RO835

<221> misc_feature
<222> (3)...(3)
<223> h = a or c or t/u at position 3

<221> misc_feature
<222> (6)...(6)
<223> y = t/u or c at position 6

<221> misc_feature
<222> (12)...(12)
<223> y = t/u or c at position 12

<221> misc_feature
<222> (27)...(27)
<223> y = t/u or c at position 27

<221> misc_feature
<222> (33)...(33)
<223> y = tu or c at position 33

<221> misc_feature
<222> (39)...(39)
<223> b = g or c or t/u at position 39

<221> misc_feature
<222> (42)...(42)
```

<223> y = t/u or c at position 42

<221> misc_feature
<222> (45)...(45)
<223> y = t/u or c at position 45

<400> 2
gghgcytccg cyaactggtg gaagcaycag cayaacgtbc aycay   45

<210> 3
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO836

<221> misc_feature
<222> (1)...(1)
<223> r = g or a at position 1

<221> misc_feature
<222> (4)...(4)
<223> r = g or a at position 4

<221> misc_feature
<222> (7)...(7)
<223> v = a or g or c at position 7

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature
<222> (19)...(19)
<223> r = g or a at position 19

<221> misc_feature
<222> (34)...(34)
<223> r = g or a at position 34

<221> misc_feature
<222> (40)...(40)
<223> r = g or a at position 40

<221> misc_feature
<222> (43)...(43)
<223> d = a or g or t/u at position 43

<400> 3
rtgrtgvacg ttrtgctgrt gcttccacca gttrgcggar gcdcc   45

<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer RO838

<221> misc_feature
<222> (6)...(6)
<223> r = g or a at position 6

<221> misc_feature
<222> (12)...(12)
<223> r = g or a at position 12

<221> misc_feature
<222> (15)...(15)
<223> y = t/u or c at position 15

<221> misc_feature
<222> (18)...(18)
<223> r = g or a at position 18

<221> misc_feature
<222> (21)...(21)
<223> r = g or a at position 21

<221> misc_feature
<222> (24)...(24)
<223> s = g or c at position 24

<221> misc_feature
<222> (27)...(27)
<223> r = g or a at position 27

<221> misc_feature
<222> (30)...(30)
<223> v = a or g or c at position 30

<400> 4
ttgatrgtct arctygtrgt rgasaarggv tggtac   36

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO753

<221> misc_feature
<222> (10)...(10)
<223> n = a or g or c or t/u, unknown, or other at
      position 10

<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature
<222> (16)...(16)

<223> n = a or g or c or t/u, unknown, or other at
      position 16

<221> misc_feature
<222> (18)...(19)
<223> r = g or a at positions 18-19

<221> misc_feature
<222> (22)...(22)
<223> r = g or a at position 22

<400> 5
catcatcatn ggraanarrt grtg   24

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO754

<221> misc_feature
<222> (15)...(15)
<223> y = t/u or c at position 15

<221> misc_feature
<222> (18)...(18)
<223> y = t/u or c at position 18

<221> misc_feature
<222> (21)...(21)
<223> n = a or g or c or t/u, unknown, or other at
      position 21

<221> misc_feature
<222> (24)...(24)
<223> y = t/u or c at position 24

<221> misc_feature
<222> (27)...(27)
<223> n = a or g or c or t/u, unknown, or other at
      position 27

<221> misc_feature
<222> (30)...(30)
<223> y = t/u or c at position 30

<400> 6
ctactactac tacaycayac ntayacnaay   30

<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer RO923

<400> 7
cggtgcagtg gtggaagaac aagcacaac   29

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO899

<400> 8
agcggataac aatttcacac aggaaacagc   30

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO939

<400> 9
cgtagtactg ctcgaggagc ttgagcgccg   30

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO898

<400> 10
cccagtcacg acgttgtaaa acgacggcca g   31

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO951

<400> 11
tcaacagaat tcatggtcca ggggcaaaag gccgagaaga tctcg   45

<210> 12
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO960

<400> 12
atacgtaagc ttttacatgg cgggaaactc cttgaagaac tcgatcg   47

<210> 13
<211> 1362
<212> DNA
<213> Saprolegnia diclina

<400> 13
atggtccagg ggcaaaaggc cgagaagatc tcgtgggcga ccatccgtga gcacaaccgc 60
caagacaacg cgtggatcgt gatccaccac aaggtgtacg acatctcggc ctttgaggac 120
cacccgggcg gcgtcgtcat gttcacgcag gccggcgaag acgcgaccga tgcgttcgct 180
gtcttccacc cgagctcggc gctcaagctc ctcgagcagt actacgtcgg cgacgtcgac 240
cagtcgacgg cggccgtcga cacgtcgatc tcggacgagg tcaagaagag ccagtcggac 300
ttcattgcgt cgtaccgcaa gctgcgcctt gaagtcaagc gcctcggctt gtacgactcg 360
agcaagctct actacctcta caagtgcgcc tcgacgctga gcattgcgct tgtgtcggcg 420
gccatttgcc tccactttga ctcgacggcc atgtacatgg tcgcggctgt catccttggc 480
ctcttttacc agcagtgcgg ctggctcgcc catgactttc tgcaccacca agtgtttgag 540
aaccacttgt ttggcgacct cgtcggcgtc atggtcggca acctctggca gggcttctcg 600
gtgcagtggt ggaagaacaa gcacaacacg caccatgcga tccccaacct ccacgcgacg 660
cccgagatcg ccttccacgg cgacccggac attgacacga tgccgattct cgcgtggtcg 720
ctcaagatgg cgcagcacgc ggtcgactcg cccgtcgggc tcttcttcat gcgctaccaa 780
gcgtacctgt actttcccat cttgctcttt gcgcgtatct cgtgggtgat ccagtcggcc 840
atgtacgcct tctacaacgt tgggcccggc ggcacctttg acaaggtcca gtacccgctg 900
ctcgagcgcg ccggcctcct cctctactac ggctggaacc tcggccttgt gtacgcagcc 960
aacatgtcgc tgctccaagc ggctgcgttc ctctttgtga gccaggcgtc gtgcggcctc 1020
ttcctcgcga tggtctttag cgtcggccac aacggcatgg aggtctttga caaggacagc 1080
aagcccgatt tttggaagct gcaagtgctc tcgacgcgca acgtgacgtc gtcgctctgg 1140
atcgactggt tcatgggcgg cctcaactac cagatcgacc accacttgtt cccgatggtg 1200
ccccggcaca acctcccggc gctcaacgtg ctcgtcaagt cgctctgcaa gcagtacgac 1260
atcccatacc acgagacggg cttcatcgcg ggcatggccg aggtcgtcgt gcacctcgag 1320
cgcatctcga tcgagttctt caaggagttt cccgccatgt aa   1362

<210> 14
<211> 453
<212> PRT
<213> Saprolegnia diclina

<400> 14

```
Met Val Gln Gly Gln Lys Ala Glu Lys Ile Ser Trp Ala Thr Ile Arg
1               5                   10                  15
Glu His Asn Arg Gln Asp Asn Ala Trp Ile Val Ile His His Lys Val
            20                  25                  30
Tyr Asp Ile Ser Ala Phe Glu Asp His Pro Gly Gly Val Val Met Phe
        35                  40                  45
Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe His Pro
    50                  55                  60
Ser Ser Ala Leu Lys Leu Leu Glu Gln Tyr Tyr Val Gly Asp Val Asp
65                  70                  75                  80
Gln Ser Thr Ala Ala Val Asp Thr Ser Ile Ser Asp Glu Val Lys Lys
                85                  90                  95
Ser Gln Ser Asp Phe Ile Ala Ser Tyr Arg Lys Leu Arg Leu Glu Val
            100                 105                 110
Lys Arg Leu Gly Leu Tyr Asp Ser Ser Lys Leu Tyr Tyr Leu Tyr Lys
        115                 120                 125
Cys Ala Ser Thr Leu Ser Ile Ala Leu Val Ser Ala Ala Ile Cys Leu
    130                 135                 140
```

```
His Phe Asp Ser Thr Ala Met Tyr Met Val Ala Ala Val Ile Leu Gly
145                 150                 155                 160
Leu Phe Tyr Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His His
                165                 170                 175
Gln Val Phe Glu Asn His Leu Phe Gly Asp Leu Val Gly Val Met Val
                180                 185                 190
Gly Asn Leu Trp Gln Gly Phe Ser Val Gln Trp Trp Lys Asn Lys His
                195                 200                 205
Asn Thr His His Ala Ile Pro Asn Leu His Ala Thr Pro Glu Ile Ala
        210                 215                 220
Phe His Gly Asp Pro Asp Ile Asp Thr Met Pro Ile Leu Ala Trp Ser
225                 230                 235                 240
Leu Lys Met Ala Gln His Ala Val Asp Ser Pro Val Gly Leu Phe Phe
                245                 250                 255
Met Arg Tyr Gln Ala Tyr Leu Tyr Phe Pro Ile Leu Leu Phe Ala Arg
                260                 265                 270
Ile Ser Trp Val Ile Gln Ser Ala Met Tyr Ala Phe Tyr Asn Val Gly
        275                 280                 285
Pro Gly Gly Thr Phe Asp Lys Val Gln Tyr Pro Leu Leu Glu Arg Ala
        290                 295                 300
Gly Leu Leu Leu Tyr Tyr Gly Trp Asn Leu Gly Leu Val Tyr Ala Ala
305                 310                 315                 320
Asn Met Ser Leu Leu Gln Ala Ala Ala Phe Leu Phe Val Ser Gln Ala
                325                 330                 335
Ser Cys Gly Leu Phe Leu Ala Met Val Phe Ser Val Gly His Asn Gly
                340                 345                 350
Met Glu Val Phe Asp Lys Asp Ser Lys Pro Asp Phe Trp Lys Leu Gln
                355                 360                 365
Val Leu Ser Thr Arg Asn Val Thr Ser Ser Leu Trp Ile Asp Trp Phe
        370                 375                 380
Met Gly Gly Leu Asn Tyr Gln Ile Asp His His Leu Phe Pro Met Val
385                 390                 395                 400
Pro Arg His Asn Leu Pro Ala Leu Asn Val Leu Val Lys Ser Leu Cys
                405                 410                 415
Lys Gln Tyr Asp Ile Pro Tyr His Glu Thr Gly Phe Ile Ala Gly Met
                420                 425                 430
Ala Glu Val Val Val His Leu Glu Arg Ile Ser Ile Glu Phe Phe Lys
                435                 440                 445
Glu Phe Pro Ala Met
        450
```

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO851

<400> 15
ccatcaagac gtaccttgcg atc

23

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO941

<400> 16
gctgaacggg tggtacgagt cgaacgtg   28

<210> 17
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO953

<400> 17
acgagagaat tcatggcccc gcagacggag ctccgccagc gc   42

<210> 18
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO956

<400> 18
aaaagactcg agttagccca tgtggatcgt ggcggcgatg ccctgc   46

<210> 19
<211> 1413
<212> DNA
<213> Saprolegnia diclina

<400> 19
atggccccgc agacggagct ccgccagcgc cacgccgccg tcgccgagac gccggtggcc 60
ggcaagaagg cctttacatg gcaggaggtc gcgcagcaca acacggcggc ctcggcctgg 120
atcattatcc gcggcaaggt ctacgacgtg accgagtggg ccaacaagca ccccggcggc 180
cgcgagatgg tgctgctgca cgccggtcgc gaggccaccg acacgttcga tcgtaccac 240
ccgttcagcg acaaggccga gtcgatcttg aacaagtatg agattggcac gttcacgggc 300
ccgtccgagt ttccgacctt caagccggac acgggcttct acaaggagtg ccgcaagcgc 360
gttggcgagt acttcaagaa gaacaacctc atccgcagg acggcttccc gggcctctgg 420
cgcatgatgg tcgtgtttgc ggtcgccggc ctcgccttgt acggcatgca cttttcgact 480
atctttgcgc tgcagctcgc ggccgcggcg ctctttggcg tctgccaggc gctgccgctg 540
ctccacgtca tgcacgactc gtcgcacgcg tcgtacacca acatgccgtt cttccattac 600
gtcgtcggcc gctttgccat ggactggttt gccggcggct cgatggtgtc atggctcaac 660
cagcacgtcg tgggccacca catctacacg aacgtcgcgg ctcggaccc ggatcttccg 720
gtcaacatgg acggcgacat ccgccgcatc gtgaaccgcc aggtgttcca gcccatgtac 780
gcattccagc acatctacct tccgccgctc tatggcgtgc ttggcctcaa gttccgcatc 840
caggacttca ccgacacgtt cggctcgcac acgaacggcc cgatccgcgt caacccgcac 900
gcgctctcga cgtggatggc catgatcagc tccaagtcgt tctgggcctt ctaccgcgtg 960
taccttccgc ttgccgtgct ccagatgccc atcaagacgt accttgcgat cttcttcctc 1020
gccgagtttg tcacgggctg gtacctcgcg ttcaacttcc aagtaagcca tgtctcgacc 1080
gagtgcggct acccatgcgg cgacgaggcc aagatggcgc tccaggacga gtgggcagtc 1140
tcgcaggtca gacgtcggt cgactacgcc catggctcgt ggatgacgac gttccttgcc 1200
ggcgcgctca actaccaggt cgtgcaccac ttgttcccca gcgtgtcgca gtaccactac 1260
ccggcgatcg cgcccatcat cgtcgacgtc tgcaaggagt acaacatcaa gtacgccatc 1320

ttgccggact ttacggcggc gttcgttgcc cacttgaagc acctccgcaa catgggccag 1380
cagggcatcg ccgccacgat ccacatgggc taa   1413

<210> 20
<211> 470
<212> PRT
<213> Saprolegnia diclina

<400> 20
```
Met Ala Pro Gln Thr Glu Leu Arg Gln Arg His Ala Ala Val Ala Glu
1               5                   10                  15
Thr Pro Val Ala Gly Lys Lys Ala Phe Thr Trp Gln Glu Val Ala Gln
            20                  25                  30
His Asn Thr Ala Ala Ser Ala Trp Ile Ile Ile Arg Gly Lys Val Tyr
        35                  40                  45
Asp Val Thr Glu Trp Ala Asn Lys His Pro Gly Gly Arg Glu Met Val
    50                  55                  60
Leu Leu His Ala Gly Arg Glu Ala Thr Asp Thr Phe Asp Ser Tyr His
65           ·       70                  75                  80
Pro Phe Ser Asp Lys Ala Glu Ser Ile Leu Asn Lys Tyr Glu Ile Gly
                85                  90                  95
Thr Phe Thr Gly Pro Ser Glu Phe Pro Thr Phe Lys Pro Asp Thr Gly
            100                 105                 110
Phe Tyr Lys Glu Cys Arg Lys Arg Val Gly Glu Tyr Phe Lys Lys Asn
            115                 120                 125
Asn Leu His Pro Gln Asp Gly Phe Pro Gly Leu Trp Arg Met Met Val
    130                 135                 140
Val Phe Ala Val Ala Gly Leu Ala Leu Tyr Gly Met His Phe Ser Thr
145                 150                 155                 160
Ile Phe Ala Leu Gln Leu Ala Ala Ala Ala Leu Phe Gly Val Cys Gln
                165                 170                 175
Ala Leu Pro Leu Leu His Val Met His Asp Ser Ser His Ala Ser Tyr
            180                 185                 190
Thr Asn Met Pro Phe Phe His Tyr Val Val Gly Arg Phe Ala Met Asp
            195                 200                 205
Trp Phe Ala Gly Gly Ser Met Val Ser Trp Leu Asn Gln His Val Val
    210                 215                 220
Gly His His Ile Tyr Thr Asn Val Ala Gly Ser Asp Pro Asp Leu Pro
225                 230                 235                 240
Val Asn Met Asp Gly Asp Ile Arg Arg Ile Val Asn Arg Gln Val Phe
                245                 250                 255
Gln Pro Met Tyr Ala Phe Gln His Ile Tyr Leu Pro Pro Leu Tyr Gly
            260                 265                 270
Val Leu Gly Leu Lys Phe Arg Ile Gln Asp Phe Thr Asp Thr Phe Gly
    275                 280                 285
Ser His Thr Asn Gly Pro Ile Arg Val Asn Pro His Ala Leu Ser Thr
    290                 295                 300
Trp Met Ala Met Ile Ser Ser Lys Ser Phe Trp Ala Phe Tyr Arg Val
305                 310                 315                 320
Tyr Leu Pro Leu Ala Val Leu Gln Met Pro Ile Lys Thr Tyr Leu Ala
                325                 330                 335
Ile Phe Phe Leu Ala Glu Phe Val Thr Gly Trp Tyr Leu Ala Phe Asn
            340                 345                 350
Phe Gln Val Ser His Val Ser Thr Glu Cys Gly Tyr Pro Cys Gly Asp
    ´355                 360                 365
Glu Ala Lys Met Ala Leu Gln Asp Glu Trp Ala Val Ser Gln Val Lys
370                 375                 380
```

Thr Ser Val Asp Tyr Ala His Gly Ser Trp Met Thr Thr Phe Leu Ala
385   390   395   400
Gly Ala Leu Asn Tyr Gln Val Val His His Leu Phe Pro Ser Val Ser
                405   410   415
Gln Tyr His Tyr Pro Ala Ile Ala Pro Ile Ile Val Asp Val Cys Lys
                420   425   430
Glu Tyr Asn Ile Lys Tyr Ala Ile Leu Pro Asp Phe Thr Ala Ala Phe
            435   440   445
Val Ala His Leu Lys His Leu Arg Asn Met Gly Gln Gln Gly Ile Ala
        450   455   460
Ala Thr Ile His Met Gly
465   470

<210> 21
<211> 914
<212> DNA
<213> Homo sapiens

<400> 21
atggaacatt ttgatgcatc acttagtacc tatttcaagg cattgctagg ccctcgagat 60
actagagtaa aaggatggtt tcttctggac aattatatac ccacatttat ctgctctgtc 120
atatatttac taattgtatg gctgggacca aaatacatga ggaataaaca gccattctct 180
tgccggggga ttttagtggt gtataacctt ggactacac tgctgtctct gtatatgttc 240
tgtgagttag taacaggagt atgggaaggc aaatacaact tcttctgtca gggcacacgc 300
accgcaggag aatcagatat gaagattatc cgtgtcctct ggtggtacta cttctccaaa 360
ctcatagaat ttatggacac tttcttcttc atcctgcgca agaacaacca ccagatcacg 420
gtcctgcacg tctaccacca tgcctcgatg ctgaacatct ggtggtttgt gatgaactgg 480
gtcccctgcg gccactctta ttttggtgcc acacttaata gcttcatcca cgtcctcatg 540
tactcttact atggtttgtc gtcagtccct tccatgcgtc cataccctg gtggaagaag 600
tacatcactc aggggcagct gcttcagttt gtgctgacaa tcatccagac cagctgcggg 660
gtcatctggc cgtgcacatt ccctcttggt tggttgtatt ccagattgg atacattatt 720
tccctgattg ctctcttcac aaacttctac attcagacct acaacaagaa aggggcctcc 780
cgaaggaaag accacctgaa ggaccaccag aatgggtccg tggctgctgt gaatggacac 840
accaacagct tttcacccct ggaaaacaat gtgaagccaa ggaagctgcg gaaggattga 900
agtcaaagaa ttga 914

<210> 22
<211> 957
<212> DNA
<213> Mortierella alpina

<400> 22
atggagtcga ttgcgccatt cctcccatca aagatgccgc aagatctgtt tatggacctt 60
gccaccgcta tcggtgtccg ggccgcgccc tatgtcgatc ctctcgaggc cgcgctggtg 120
gcccaggccg agaagtacat ccccacgatt gtccatcaca cgcgtgggtt cctggtcgcg 180
gtggagtcgc ctttggcccg tgagctgccg ttgatgaacc cgttccacgt gctgttgatc 240
gtgctcgctt atttggtcac ggtctttgtg ggcatgcaga tcatgaagaa ctttgagcgg 300
ttcgaggtca agacgttttc gctcctgcac aacttttgtc tggtctcgat cagcgcctac 360
atgtgcggtg ggatcctgta cgaggcttat caggccaact atggactgtt tgagaacgct 420
gctgatcata ccttcaaggg tcttcctatg ccaagatga tctggctctt ctacttctcc 480
aagatcatgg agtttgtcga caccatgatc atggtcctca gaagaacaa ccgccagatc 540
tccttcttgc acgtttacca ccacagctcc atcttcacca tctggtggtt ggtcaccttt 600
gttgcaccca acggtgaagc ctacttctct gctgcgttga ctcgttcat ccatgtgatc 660
atgtacggct actacttctt gtcggccttg gcttcaagc aggtgtcgtt catcaagttc 720
tacatcacgc gctcgcagat gacacagttc tgcatgatgt cggtccagtc ttcctgggac 780
atgtacgcca tgaaggtcct tggccgcccc ggatacccct tcttcatcac ggctctgctt 840

```
tggttctaca tgtggaccat gctcggtctc ttctacaact tttacagaaa gaacgccaag 900
ttggccaagc aggccaaggc cgacgctgcc aaggagaagg caaggaagtt gcagtaa    957
```

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO936

<400> 23
```
gtcgggcaag gcggaaaagt acctcaagag                                  30
```

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO937

<400> 24
```
aaacctgtag acaatgtgga ggggcgtggg                                  30
```

<210> 25
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO972

<400> 25
```
atacttgaat tcatgggacg cggcggcgaa ggtcaggtga ac                    42
```

<210> 26
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO949

<400> 26
```
cttatactcg agctaagcgg ccttggccgc cgcctggcc                        39
```

<210> 27
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO950

<400> 27
```
cttatactcg agtaaatggc tcgcgaggcg aagcgagtgg c                     41
```

<210> 28
<211> 1320
<212> DNA
<213> Thraustochytrium aureum

<400> 28
```
atgggacgcg gcggcgaagg tcaggtgaac agcgcgcagg tggcacaagg cggtgcggga 60
acgcgaaaga cgatcctgat cgagggcgag gtctacgatg tcaccaactt taggcacccc 120
ggcgggtcga tcatcaagtt tctcacgacc gacggcaccg aggctgtgga cgcgacgaac 180
gcgtttcgcg agtttcactg ccggtcgggc aaggcggaaa agtacctcaa gagcctgccc 240
aagctcggcg cgccgagcaa gatgaagttt gacgccaagg agcaggcccg cgcgacgcg 300
atcacgcgag actacgtcaa gctgcgcgag gagatggtgg ccgagggcct cttcaagccc 360
gcgcccctcc acattgtcta caggtttgcg gagatcgcag ccctgttcgc ggcctcgttc 420
tacctgtttt cgatgcgcgg aaacgtgttc gccacgctcg cggccatcgc agtcggggc 480
atcgcgcagg ccgctgcgg ctggctcatg cacgagtgcg gacacttctc gatgaccggg 540
tacatcccgc ttgacgtgcg cctgcaggag ctggtgtacg gcgtggggtg ctcgatgtcg 600
gcgagctggt ggcgcgttca gcacaacaag caccacgcga ccccgcagaa actcaagcac 660
gacgtcgacc tcgacaccct gccgctcgtt gcgttcaacg agaagatcgc cgccaaggtg 720
cgccccggct cgttccaggc caagtggctc tcggcgcagg cgtacatttt tgcgccggtg 780
tcctgcttcc tggttggtct cttctggacc ctgtttctgc acccgcgcca catgccgcgc 840
acgagccact ttgctgagat ggccgccgtc gcggtgcgcg tcgtgggctg gcggcgctc 900
atgcactcgt tcgggtacag cgggagcgac tcgttcggtc tctacatggc cacctttggc 960
tttggctgca cctacatctt caccaacttt gcggtcagcc acacgcacct cgacgtcacc 1020
gagccggacg agttcctgca ctgggtcgag tacgccgcgc tgcacacgac caacgtgtcc 1080
aacgactcgt ggttcatcac ctggtggatg tcgtacctca actttcagat cgagcaccac 1140
ctctttccgt cgctgcccca gctcaacgcc ccgcgcgtcg ccccgcgcgt ccgcgccctc 1200
ttcgagaagc acggcatggc ttacgacgag cgccgtacc ttaccgcgct ggcgacacg 1260
tttgccaacc tgcacgccgt gggccaaaac gcgggccagg cggcggccaa ggccgcttag 1320
```

<210> 29
<211> 439
<212> PRT
<213> Thraustochytrium aureum

<400> 29
```
Met Gly Arg Gly Gly Glu Gly Gln Val Asn Ser Ala Gln Val Ala Gln
  1               5                  10                  15
Gly Gly Ala Gly Thr Arg Lys Thr Ile Leu Ile Glu Gly Glu Val Tyr
             20                  25                  30
Asp Val Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Phe Leu
             35                  40                  45
Thr Thr Asp Gly Thr Glu Ala Val Asp Ala Thr Asn Ala Phe Arg Glu
        50                  55                  60
Phe His Cys Arg Ser Gly Lys Ala Glu Lys Tyr Leu Lys Ser Leu Pro
65                  70                  75                  80
Lys Leu Gly Ala Pro Ser Lys Met Lys Phe Asp Ala Lys Glu Gln Ala
                 85                  90                  95
Arg Arg Asp Ala Ile Thr Arg Asp Tyr Val Lys Leu Arg Glu Glu Met
            100                 105                 110
Val Ala Glu Gly Leu Phe Lys Pro Ala Pro Leu His Ile Val Tyr Arg
            115                 120                 125
Phe Ala Glu Ile Ala Ala Leu Phe Ala Ala Ser Phe Tyr Leu Phe Ser
        130                 135                 140
Met Arg Gly Asn Val Phe Ala Thr Leu Ala Ala Ile Ala Val Gly Gly
145                 150                 155                 160
```

```
Ile Ala Gln Gly Arg Cys Gly Trp Leu Met His Glu Cys Gly His Phe
            165             170             175
Ser Met Thr Gly Tyr Ile Pro Leu Asp Val Arg Leu Gln Glu Leu Val
            180             185             190
Tyr Gly Val Gly Cys Ser Met Ser Ala Ser Trp Trp Arg Val Gln His
            195             200             205
Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp Leu
    210             215             220
Asp Thr Leu Pro Leu Val Ala Phe Asn Glu Lys Ile Ala Ala Lys Val
225             230             235             240
Arg Pro Gly Ser Phe Gln Ala Lys Trp Leu Ser Ala Gln Ala Tyr Ile
            245             250             255
Phe Ala Pro Val Ser Cys Phe Leu Val Gly Leu Phe Trp Thr Leu Phe
            260             265             270
Leu His Pro Arg His Met Pro Arg Thr Ser His Phe Ala Glu Met Ala
            275             280             285
Ala Val Ala Val Arg Val Val Gly Trp Ala Ala Leu Met His Ser Phe
    290             295             300
Gly Tyr Ser Gly Ser Asp Ser Phe Gly Leu Tyr Met Ala Thr Phe Gly
305             310             315             320
Phe Gly Cys Thr Tyr Ile Phe Thr Asn Phe Ala Val Ser His Thr His
            325             330             335
Leu Asp Val Thr Glu Pro Asp Glu Phe Leu His Trp Val Glu Tyr Ala
            340             345             350
Ala Leu His Thr Thr Asn Val Ser Asn Asp Ser Trp Phe Ile Thr Trp
    355             360             365
Trp Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Ser
    370             375             380
Leu Pro Gln Leu Asn Ala Pro Arg Val Ala Pro Arg Val Arg Ala Leu
385             390             395             400
Phe Glu Lys His Gly Met Ala Tyr Asp Glu Arg Pro Tyr Leu Thr Ala
            405             410             415
Leu Gly Asp Thr Phe Ala Asn Leu His Ala Val Gly Gln Asn Ala Gly
            420             425             430
Gln Ala Ala Ala Lys Ala Ala
            435
```

<210> 30
<211> 1338
<212> DNA
<213> Thraustochytrium aureum

<400> 30
```
gaattcacca tgggtcgcgg agcacaggga gagccaaggc aggccacaga gctgaagagc    60
agcccaagtg agcagcgtaa ggtgttgctc attgacgggc agctgtacga tgcaaccaac   120
ttcaggcatc ctggtggctc catcatcaaa tatttgtgca ccgatggcaa ggaggtagtt   180
gatgcaaccg aagcgtacaa ggagttccac tgcagatcct cgaaggcggt caagtacctc   240
aactccctgc aaagatcga cggcccaatc aagtacaaat acgacgcaaa ggagcaggct   300
cgccatgaca aactcacgag ggagtatgta gctctccgcg aacagctcgt caaggaggga   360
tactttgacc ccagcccgct ccacattatc tacagatgcg ccgagttggc agccatgttc   420
gctctctcgt tctacctttt ctccttcaag ggtaacgtca tggccactat tgctgccatc   480
gtgattgggg ggtgcgtgca gggtcgttgt gggtggctca tgcatgaagc tggccactac   540
agcatgaccg aaacatccc tgttgacttg cgccttcaag agtttttgta cggaattggg   600
tgtggcatga gcggggcttg gtggagaagc cagcacaaca agcaccacgc cacccccaa   660
aagctcaagc atgacgttga tttggacact cttcctcttg tcgcctggaa cgagaaaatt   720
gcccgtcgcg tcaagccagg tagcttccag gcaaagtggc ttcatctcca gggatacatc   780
```

```
tttgccccag tctcctgcct tctcgttggt ctcttctgga ctttgtactt gcatcctcgc      840
cacatgatcc gcaccaagcg caacttcgag atattttctg tcgctctgcg ctacgtatgc      900
tggttctcgc ttcttttgag catgggctac actgtcggag agtctctggg tctctatgtg      960
cttacttttg acttggctg  tacctacatc tttacgcatt ttgctgtaag ccacacccac     1020
ttgccagtgt ccgaggagga cgagtacctg cactgggtcg agtacgctgc gctgcacacc     1080
acgaacgttg ccatcgactc gtacgttgtc acctggctga tgagctacct caactttcag     1140
atcgagcacc acttgttccc ttgctgcccg cagttccgcc accctgcaat ctcttctcgc     1200
gtcaagaaac ttttcgagga caatggtctg gtatacgacg cccgctcata cgtccaggcg     1260
ctcaaggata ccttcggcaa cctacacgaa gtgggcgtca acgctggcca agctgccaag     1320
agcgagtaag atctcgag                                                   1338
```

<210> 31
<211> 439
<212> PRT
<213> Thraustochytrium aureum

<400> 31

```
Met Gly Arg Gly Ala Gln Gly Glu Pro Arg Gln Ala Thr Glu Leu Lys
 1               5                  10                  15
Ser Ser Pro Ser Glu Gln Arg Lys Val Leu Leu Ile Asp Gly Gln Leu
            20                  25                  30
Tyr Asp Ala Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Tyr
        35                  40                  45
Leu Cys Thr Asp Gly Lys Glu Val Val Asp Ala Thr Glu Ala Tyr Lys
    50                  55                  60
Glu Phe His Cys Arg Ser Ser Lys Ala Val Lys Tyr Leu Asn Ser Leu
65                  70                  75                  80
Pro Lys Ile Asp Gly Pro Ile Lys Tyr Lys Tyr Asp Ala Lys Glu Gln
                85                  90                  95
Ala Arg His Asp Lys Leu Thr Arg Glu Tyr Val Ala Leu Arg Glu Gln
            100                 105                 110
Leu Val Lys Glu Gly Tyr Phe Asp Pro Ser Pro Leu His Ile Ile Tyr
        115                 120                 125
Arg Cys Ala Glu Leu Ala Ala Met Phe Ala Leu Ser Phe Tyr Leu Phe
    130                 135                 140
Ser Phe Lys Gly Asn Val Met Ala Thr Ile Ala Ala Ile Val Ile Gly
145                 150                 155                 160
Gly Cys Val Gln Gly Arg Cys Gly Trp Leu Met His Glu Ala Gly His
                165                 170                 175
Tyr Ser Met Thr Gly Asn Ile Pro Val Asp Leu Arg Leu Gln Glu Phe
            180                 185                 190
Leu Tyr Gly Ile Gly Cys Gly Met Ser Gly Ala Trp Trp Arg Ser Gln
        195                 200                 205
His Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp
    210                 215                 220
Leu Asp Thr Leu Pro Leu Val Ala Trp Asn Glu Lys Ile Ala Arg Arg
225                 230                 235                 240
Val Lys Pro Gly Ser Phe Gln Ala Lys Trp Leu His Leu Gln Gly Tyr
                245                 250                 255
Ile Phe Ala Pro Val Ser Cys Leu Leu Val Gly Leu Phe Trp Thr Leu
            260                 265                 270
Tyr Leu His Pro Arg His Met Ile Arg Thr Lys Arg Asn Phe Glu Ile
        275                 280                 285
Phe Ser Val Ala Leu Arg Tyr Val Cys Trp Phe Ser Leu Leu Leu Ser
    290                 295                 300
Met Gly Tyr Thr Val Gly Glu Ser Leu Gly Leu Tyr Val Leu Thr Phe
305                 310                 315                 320
```

```
Gly Leu Gly Cys Thr Tyr Ile Phe Thr His Phe Ala Val Ser His Thr
              325             330                         335
His Leu Pro Val Ser Glu Glu Asp Glu Tyr Leu His Trp Val Glu Tyr
              340             345                         350
Ala Ala Leu His Thr Thr Asn Val Ala Ile Asp Ser Tyr Val Val Thr
              355             360                         365
Trp Leu Met Ser Tyr Leu Asn Phe Gln Ile Glu His His Leu Phe Pro
      370             375             380
Cys Cys Pro Gln Phe Arg His Pro Ala Ile Ser Ser Arg Val Lys Lys
385                 390             395                     400
Leu Phe Glu Asp Asn Gly Leu Val Tyr Asp Ala Arg Ser Tyr Val Gln
                  405             410                     415
Ala Leu Lys Asp Thr Phe Gly Asn Leu His Glu Val Gly Val Asn Ala
              420             425                     430
Gly Gln Ala Ala Lys Ser Glu
              435
```

```
<210> 32
<211> 1381
<212> DNA
<213> Thraustochytrium aureum

<400> 32
ccatgggccg cggcggcgag aaaagcgagg tggaccaggt gcagccacaa aagaccgagc      60
agctccagaa ggccaagtgg gaggatgttg ttcgcatcaa tggagtcgaa tacgacgtca     120
cggactatct cagaaaacac cctggtggca gcgtgatcaa gtacgggctt gccaacaccg     180
gcgctgatgc cacgtccctc tttgaagcgt tccacatgcg ctcaaagaag gctcagatgg     240
tgctcaagtc tctcccaaag cgtgctccgg tcctcgagat ccagccaaac cagcttccag     300
aggagcagac caaggaggcg gagatgctgc gtgattttaa aaaatttgag gatgagattc     360
gccgggatgg attgatggaa ccttccttct ggcatcgcgc ttacagatta tcagagcttg     420
taggtatgtt cacgctcggc ctctacctct ctcgttaaa cactcctctg tctattgctg     480
ctggtgtcct cgtccacggt ctctttggtg cattctgtgg atggtgccag catgaggcag     540
gccacggctc ctttttttac agcctttggt ggggcaagcg tgtacaggcc atgttgatcg     600
ggtttggtct aggaacatcc ggcgacatgt ggaacatgat gcacaacaag catcatgctg     660
ccacccaaaa ggttcatcac gaccttgaca ttgacacaac tccttttgta gctttcttca     720
acactgcatt tgagaaaaac agatggaagg cttttccaa ggcttgggtc cgctttcagg     780
cttttcacgtt cattcctgtc accagcggca tgatcgtcat gctgttctgg ctgtttttc      840
tccaccctcg ccgcgtcgtt caaaagaaga actttgagga gggtttttgg atgctgtcga     900
gccacattgt gcgcacctat ctcttccacc ttgtgaccgg ctgggagagc ctcgctgcat     960
gctaccttgt tgggtattgg gcgtgcatgt gggtgtccgg tatgtatttg tttggccact    1020
tttcgctctc ccacactcat atggacattg tggaggcgga cgtgcataag aactgggtca    1080
ggtacgctgt tgaccacact gttgacatca gcccatccaa cccgctcgtg tgctgggtca    1140
tgggttacct caacatgcag accatccacc acttgtggcc tgccatgccc cagtaccacc    1200
aggtcgaggt ctcacgccgc tttgccatct tcgccaaaaa acacggcctc aactaccgcg    1260
tcgtctctta ctttgaggct tggcgcctga tgctccaaaa tcttgctgac gtcggttccc    1320
actaccatga gaacggtgtc aagcgcgccc caaagaaagc caaggcgcag tagaaagcta    1380
t                                                                    1381
```

```
<210> 33
<211> 456
<212> PRT
<213> Thraustochytrium aureum

<400> 33
Met Gly Arg Gly Gly Glu Lys Ser Glu Val Asp Gln Val Gln Pro Gln
  1               5                 10                    15
Lys Thr Glu Gln Leu Gln Lys Ala Lys Trp Glu Asp Val Val Arg Ile
```

```
                    20                    25                    30
Asn Gly Val Glu Tyr Asp Val Thr Asp Tyr Leu Arg Lys His Pro Gly
        35              40                  45
Gly Ser Val Ile Lys Tyr Gly Leu Ala Asn Thr Gly Ala Asp Ala Thr
        50                  55                  60
Ser Leu Phe Glu Ala Phe His Met Arg Ser Lys Lys Ala Gln Met Val
65                      70                  75                  80
Leu Lys Ser Leu Pro Lys Arg Ala Pro Val Leu Glu Ile Gln Pro Asn
                85                  90                  95
Gln Leu Pro Glu Glu Gln Thr Lys Glu Ala Glu Met Leu Arg Asp Phe
            100                 105                 110
Lys Lys Phe Glu Asp Glu Ile Arg Arg Asp Gly Leu Met Glu Pro Ser
        115                 120                 125
Phe Trp His Arg Ala Tyr Arg Leu Ser Glu Leu Val Gly Met Phe Thr
        130                 135                 140
Leu Gly Leu Tyr Leu Phe Ser Leu Asn Thr Pro Leu Ser Ile Ala Ala
145                 150                 155                 160
Gly Val Leu Val His Gly Leu Phe Gly Ala Phe Cys Gly Trp Cys Gln
                165                 170                 175
His Glu Ala Gly His Gly Ser Phe Phe Tyr Ser Leu Trp Trp Gly Lys
            180                 185                 190
Arg Val Gln Ala Met Leu Ile Gly Phe Gly Leu Gly Thr Ser Gly Asp
        195                 200                 205
Met Trp Asn Met Met His Asn Lys His His Ala Ala Thr Gln Lys Val
    210                 215                 220
His His Asp Leu Asp Ile Asp Thr Thr Pro Phe Val Ala Phe Phe Asn
225                 230                 235                 240
Thr Ala Phe Glu Lys Asn Arg Trp Lys Gly Phe Ser Lys Ala Trp Val
                245                 250                 255
Arg Phe Gln Ala Phe Thr Phe Ile Pro Val Thr Ser Gly Met Ile Val
            260                 265                 270
Met Leu Phe Trp Leu Phe Phe Leu His Pro Arg Arg Val Val Gln Lys
        275                 280                 285
Lys Asn Phe Glu Glu Gly Phe Trp Met Leu Ser Ser His Ile Val Arg
    290                 295                 300
Thr Tyr Leu Phe His Leu Val Thr Gly Trp Glu Ser Leu Ala Ala Cys
305                 310                 315                 320
Tyr Leu Val Gly Tyr Trp Ala Cys Met Trp Val Ser Gly Met Tyr Leu
                325                 330                 335
Phe Gly His Phe Ser Leu Ser His Thr His Met Asp Ile Val Glu Ala
            340                 345                 350
Asp Val His Lys Asn Trp Val Arg Tyr Ala Val Asp His Thr Val Asp
        355                 360                 365
Ile Ser Pro Ser Asn Pro Leu Val Cys Trp Val Met Gly Tyr Leu Asn
    370                 375                 380
Met Gln Thr Ile His His Leu Trp Pro Ala Met Pro Gln Tyr His Gln
385                 390                 395                 400
Val Glu Val Ser Arg Arg Phe Ala Ile Phe Ala Lys Lys His Gly Leu
            405                 410                 415
Asn Tyr Arg Val Val Ser Tyr Phe Glu Ala Trp Arg Leu Met Leu Gln
        420                 425                 430
Asn Leu Ala Asp Val Gly Ser His Tyr His Glu Asn Gly Val Lys Arg
        435                 440                 445
Ala Pro Lys Lys Ala Lys Ala Gln
    450                 455
```

<210> 34

<211> 1329
<212> DNA
<213> Isochrysis galbana

<400> 34
```
atggtggcag gcaaatcagg cgctgcggcg cacgtgactc acagctcgac attgccccgt      60
gagtaccatg gcgcgaccaa cgactcgcgc tctgaggcgg ccgacgtcac cgtctctagc     120
atcgatgctg aaaaggagat gatcatcaac ggccgcgtgt atgacgtgtc gtcatttgtg     180
aagcggcacc caggtggctc ggtgatcaag ttccagctgg gcgccgacgc gagcgacgcg     240
tacaacaact ttcacgtccg ctccaagaag gcggacaaga tgctgtattc gctcccgtcc     300
cggccggccg aggccggcta cgcccaggac gacatctccc gcgactttga gaagctgcgc     360
ctcgagctga aggaggaggg ctacttcgag cccaacctgg tgcacgtgag ctacaggtgt     420
gtggaggttc ttgccatgta ctgggctggc gtccagctca tctggtccgg gtactggttc     480
ctcggcgcga tcgtggccgg cattgcgcag ggccgctgcg gctggctcca gcatgagggt     540
gggcactact cgctcaccgg caacatcaag atcgaccggc atctgcagat ggccatctat     600
gggcttggct gcggcatgtc gggctgctac tggcgcaacc agcacaacaa gcaccacgcc     660
acgccgcaga agctcgggac cgaccccgac ctgcagacga tgccgctggt ggccttccac     720
aagatcgtcg cgccaaggc gcgaggcaag ggcaaggcgt ggctggcgtg gcaggcgccg     780
ctcttctttg cgggatcat ctgctcgctc gtctctttcg gctggcagtt cgtgctccac     840
cccaaccacg cgctgcgcgt gcacaatcac ctggagctcg cgtacatggg cctgcggtac     900
gtgctgtggc acctggcctt tggccacctc gggctgctga gctcgctccg cctgtacgcc     960
ttttacgtgg ccgtgggcgg cacctacatc ttcaccaact cgccgtctc gcacacccac    1020
aaggacgtcg tcccgcccac caagcacatc tcgtgggcac tctactcggc caaccacacg    1080
accaactgct ccgactcgcc ctttgtcaac tggtggatgg cctacctcaa cttccagatc    1140
gagcaccacc tcttcccgtc gatgccgcag tacaaccacc ccaagatcgc cccgcgggtg    1200
cgcgcgctct cgagaagca cggggtcgag tatgacgtcc ggccatacct ggagtgtttt    1260
cgggtcacgt acgtcaacct gctcgccgta ggcaacccgg agcactccta ccacgagcac    1320
acgcactag                                                            1329
```

<210> 35
<211> 442
<212> PRT
<213> Isochrysis galbana

<400> 35
```
Met Val Ala Gly Lys Ser Gly Ala Ala Ala His Val Thr His Ser Ser
1               5                   10                  15
Thr Leu Pro Arg Glu Tyr His Gly Ala Thr Asn Asp Ser Arg Ser Glu
            20                  25                  30
Ala Ala Asp Val Thr Val Ser Ser Ile Asp Ala Glu Lys Glu Met Ile
        35                  40                  45
Ile Asn Gly Arg Val Tyr Asp Val Ser Ser Phe Val Lys Arg His Pro
    50                  55                  60
Gly Gly Ser Val Ile Lys Phe Gln Leu Gly Ala Asp Ala Ser Asp Ala
65                  70                  75                  80
Tyr Asn Asn Phe His Val Arg Ser Lys Lys Ala Asp Lys Met Leu Tyr
                85                  90                  95
Ser Leu Pro Ser Arg Pro Ala Glu Ala Gly Tyr Ala Gln Asp Asp Ile
            100                 105                 110
Ser Arg Asp Phe Glu Lys Leu Arg Leu Glu Leu Lys Glu Glu Gly Tyr
        115                 120                 125
Phe Glu Pro Asn Leu Val His Val Ser Tyr Arg Cys Val Glu Val Leu
    130                 135                 140
Ala Met Tyr Trp Ala Gly Val Gln Leu Ile Trp Ser Gly Tyr Trp Phe
145                 150                 155                 160
Leu Gly Ala Ile Val Ala Gly Ile Ala Gln Gly Arg Cys Gly Trp Leu
                165                 170                 175
```

```
Gln His Glu Gly Gly His Tyr Ser Leu Thr Gly Asn Ile Lys Ile Asp
            180             185             190
Arg His Leu Gln Met Ala Ile Tyr Gly Leu Gly Cys Gly Met Ser Gly
        195             200             205
Cys Tyr Trp Arg Asn Gln His Asn Lys His His Ala Thr Pro Gln Lys
    210             215             220
Leu Gly Thr Asp Pro Asp Leu Gln Thr Met Pro Leu Val Ala Phe His
225             230             235             240
Lys Ile Val Gly Ala Lys Ala Arg Gly Lys Gly Lys Ala Trp Leu Ala
            245             250             255
Trp Gln Ala Pro Leu Phe Phe Gly Gly Ile Ile Cys Ser Leu Val Ser
            260             265             270
Phe Gly Trp Gln Phe Val Leu His Pro Asn His Ala Leu Arg Val His
        275             280             285
Asn His Leu Glu Leu Ala Tyr Met Gly Leu Arg Tyr Val Leu Trp His
    290             295             300
Leu Ala Phe Gly His Leu Gly Leu Leu Ser Ser Leu Arg Leu Tyr Ala
305             310             315             320
Phe Tyr Val Ala Val Gly Gly Thr Tyr Ile Phe Thr Asn Phe Ala Val
            325             330             335
Ser His Thr His Lys Asp Val Val Pro Pro Thr Lys His Ile Ser Trp
        340             345             350
Ala Leu Tyr Ser Ala Asn His Thr Thr Asn Cys Ser Asp Ser Pro Phe
        355             360             365
Val Asn Trp Trp Met Ala Tyr Leu Asn Phe Gln Ile Glu His His Leu
    370             375             380
Phe Pro Ser Met Pro Gln Tyr Asn His Pro Lys Ile Ala Pro Arg Val
385             390             395             400
Arg Ala Leu Phe Glu Lys His Gly Val Glu Tyr Asp Val Arg Pro Tyr
            405             410             415
Leu Glu Cys Phe Arg Val Thr Tyr Val Asn Leu Leu Ala Val Gly Asn
            420             425             430
Pro Glu His Ser Tyr His Glu His Thr His
        435             440
```

<210> 36
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO838

<221> misc_feature
<222> (7)...(7)
<223> v = a or g or c at position 7

<221> misc_feature
<222> (10)...(10)
<223> r = g or a at position 10

<221> misc_feature
<222> (13)...(13)
<223> s = g or c at position 13

<221> misc_feature
<222> (16)...(16)

<223> r = g or a at position 16

<221> misc_feature
<222> (19)...(19)
<223> r = g or a at position 19

<221> misc_feature
<222> (22)...(22)
<223> y = t/u or c at position 22

<221> misc_feature
<222> (25)...(25)
<223> r = g or a at position 25

<221> misc_feature
<222> (31)...(31)
<223> r = g or a at position 31

<400> 36
catggtvggr aasagrtgrt gytcratctg rtagtt   36

<210> 37
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1065

<400> 37
cgacaagagg aagagtgtcc aaatc   25

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1064

<400> 38
cgccttcaag agtttttgta cggaattggg   30

<210> 39
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1097

<400> 39
cttgtaccat gggtcgcgga gcacagggag   30

<210> 40
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer RO1098

<400> 40
tgaagcttac tcgctcttgg cagcttggcc   30

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1107

<400> 41
tttaaccatg ggccgcggcg gcgagaaaag   30

<210> 42
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1108

<400> 42
gggaagaagc tttctactgc gccttggctt tctttg   36

<210> 43
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1235

<400> 43
cgaagttggt gaagatgtag gtgccg   26

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1232

<400> 44
gagcgacgcg tacaacaact ttcacgt   27

<210> 45
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 45
cgactggagc acgaggacac tga   23

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> GeneRacer 3 Prime Primer

<400> 46
gctgtcaacg atacgctacg taacg   25

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Nested Primer RO1234

<400> 47
agctccaggt gattgtgcac gcgcag   26

<210> 48
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1233

<400> 48
gactttgaga agctgcgcct cgagctg   27

<210> 49
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Nested 5 Prime Primer

<400> 49
ggacactgac atggactgaa ggagta   26

<210> 50
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Nested 3 Prime Primer

<400> 50
cgctacgtaa cggcatgaca gtg   23

<210> 51
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1309

<400> 51
atgatggaat tcatggtggc aggcaaatca ggcgc   35

<210> 52
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer RO1310

<400> 52
aataatgtcg acctagtgcg tgtgctcgtg gtagg   35

<210> 53
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Peptide Sequence

<400> 53
Val Tyr Asp Val Thr Glu Trp Val Lys Arg His Pro Gly Gly
 1   5   10

<210> 54
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Peptide Sequence

<400> 54
Gly Ala Ser Ala Asn Trp Trp Lys His Gln His Asn Val His His
 1   5   10   15

<210> 55
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Peptide Sequence

<400> 55
Asn Tyr Gln Ile Glu His His Leu Phe Pro Thr Met
 1   5   10